

A1 structure visualization; and computer functionality for protein sequence and structural analysis; and database searching tools.

A2 ~~Sub C6~~ 28. (Amended) The method of claim 1, further after generating the 3-D structural variant models, exporting some or all of the[m] models into a program that computationally docks the models with test compounds to assess intermolecular interactions.

A3 ~~AT~~ ~~F18~~ 49 48. (Amended) The method of claim ~~44~~ 45, wherein the target is enzyme expressed by [a] an infectious agent.

A4 54. (Amended) A database, comprising:
sequences of nucleotides encoding a protein or portions thereof, wherein proteins comprise polymorphic variants; and the portions encode a domain of the protein that comprises a site in the protein that binds to a drug candidate[s]; and the coordinates of 3-dimensional (3-D) structures of the encoded proteins or portions thereof.

A5 56. (Amended) The database of claim 53 that comprises [at] more than 10, more than 100, more than 1000, more than 8000, or more than 10,000 polymorphic variants and the corresponding 3-D structures.

REMARKS

Any fees that may be due in connection with filing this paper, or during the entire pendency of this application, may be charged to Deposit Account No. 50-1213.

The amendments to the specification and to claims 7, 8, 21, 27, 48, and 56 correct obvious typographical errors, correct citations of publications, and produce

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Preliminary Amendment**

grammatical clarity. The amendment to claim 23 corrects a typographical error and finds basis in claim 12.

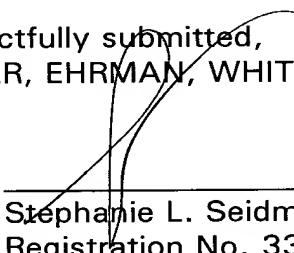
No new matter has been added.

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Entry of this amendment and examination of the application are respectfully requested.

Respectfully submitted,
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